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<110> Li, Limin
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 ggacaacctg gccagcagg agcaggacgt cctctaccgc cgctgaagc tcttcaccca 1500
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 aacgaaacac gccatctgca aactccagga gcagatatc cacctgcaga tgaaacttat 1620

tgaacaggat ctgtgtcgag agcgggtctgg gaggagagca aagggcaaga agagtgactc 1680
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 cctcagccca gtcacaactg ccatttccag tctctgctga gtgtcccaga ccctcgaggc 2700
 tgccactccg tcgtgggtttt atttttaata tagagagagt tttgaattct 2750

<210> 6
 <211> 850
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Val Pro Thr Ala Ala Ile Ala Val Gly Gly Tyr Phe Leu Gly Gly
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Met Glu Glu Lys Arg Arg Lys Tyr Ser Ile Ser Ser Asp Asn Ser Asp
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Thr Thr Asp Ser His Ala Thr Ser Thr Ser Ala Ser Arg Cys Ser Lys
 35 40 45

Leu Pro Ser Ser Thr Lys Ser Gly Trp Pro Arg Gln Asn Glu Lys Lys
 50 55 60

Pro Ser Glu Val Phe Arg Thr Asp Leu Ile Thr Ala Met Lys Ile Pro
65 70 75 80

Asp Ser Tyr Gln Leu Ser Pro Asp Asp Tyr Tyr Ile Leu Ala Asp Pro
85 90 95

Trp Arg Gln Glu Trp Glu Lys Gly Val Gln Val Pro Ala Gly Ala Glu
100 105 110

Ala Ile Pro Glu Pro Val Val Arg Ile Leu Pro Pro Leu Glu Gly Pro
115 120 125

Pro Ala Gln Ala Ser Pro Ser Ser Thr Met Leu Gly Glu Gly Ser Gln
130 135 140

Pro Asp Trp Pro Gly Gly Ser Arg Tyr Asp Leu Asp Glu Ile Asp Ala
145 150 155 160

Tyr Trp Leu Glu Leu Ile Asn Ser Glu Leu Lys Glu Met Glu Arg Pro
165 170 175

Glu Leu Asp Glu Leu Thr Leu Glu Arg Val Leu Glu Glu Leu Glu Thr
180 185 190

Leu Cys His Gln Asn Met Ala Arg Ala Ile Glu Thr Gln Glu Gly Leu
195 200 205

Gly Ile Glu Tyr Asp Glu Asp Val Val Cys Asp Val Cys Arg Ser Pro
210 215 220

Glu Gly Glu Asp Gly Asn Glu Met Val Phe Cys Asp Lys Cys Asn Val
225 230 235 240

Cys Val His Gln Ala Cys Tyr Gly Ile Leu Lys Val Pro Thr Gly Ser
245 250 255

Trp Leu Cys Arg Thr Cys Ala Leu Gly Val Gln Pro Lys Cys Leu Leu
260 265 270

Cys Pro Lys Arg Gly Gly Ala Leu Lys Pro Thr Arg Ser Gly Thr Lys
275 280 285

Trp Val His Val Ser Cys Ala Leu Trp Ile Pro Glu Val Ser Ile Gly
290 295 300

Cys Pro Glu Lys Met Glu Pro Ile Thr Lys Ile Ser His Ile Pro Ala
 305 310 315 320

Ser Arg Trp Ala Leu Ser Cys Ser Leu Cys Lys Glu Cys Thr Gly Thr
 325 330 335

Cys Ile Gln Cys Ser Met Pro Ser Cys Val Thr Ala Phe His Val Thr
 340 345 350

Cys Ala Phe Asp His Gly Leu Glu Met Arg Thr Ile Leu Ala Asp Asn
 355 360 365

Asp Glu Val Lys Phe Lys Ser Phe Cys Gln Glu His Ser Asp Gly Gly
 370 375 380

Pro Arg Asn Glu Pro Thr Ser Glu Pro Thr Glu Pro Ser Gln Ala Gly
 385 390 395 400

Glu Asp Leu Glu Lys Val Thr Leu Arg Lys Gln Arg Leu Gln Gln Leu
 405 410 415

Glu Glu Asp Phe Tyr Glu Leu Val Glu Pro Ala Glu Val Ala Glu Arg
 420 425 430

Leu Asp Leu Ala Glu Ala Leu Val Asp Phe Ile Tyr Gln Tyr Trp Lys
 435 440 445

Leu Lys Arg Lys Ala Asn Ala Asn Gln Pro Leu Leu Thr Pro Lys Thr
 450 455 460

Asp Glu Val Asp Asn Leu Ala Gln Gln Glu Gln Asp Val Leu Tyr Arg
 465 470 475 480

Arg Leu Lys Leu Phe Thr His Leu Arg Gln Asp Leu Glu Arg Val Arg
 485 490 495

Asn Leu Cys Tyr Met Val Thr Arg Arg Glu Arg Thr Lys His Ala Ile
 500 505 510

Cys Lys Leu Gln Glu Gln Ile Phe His Leu Gln Met Lys Leu Ile Glu
 515 520 525

Gln Asp Leu Cys Arg Glu Arg Ser Gly Arg Arg Ala Lys Gly Lys Lys
 530 535 540

Ser Asp Ser Lys Arg Lys Gly Cys Glu Gly Ser Lys Gly Ser Thr Glu
 545 550 555 560

Lys Lys Glu Lys Val Lys Ala Gly Pro Asp Ser Val Leu Gly Gln Leu
 565 570 575

Ala Gly Leu Ser Thr Ser Phe Pro Ile Asp Gly Thr Phe Phe Asn Ser
 580 585 590

Trp Leu Ala Gln Ser Val Gln Ile Thr Ala Glu Asn Met Ala Met Ser
 595 600 605

Glu Trp Pro Leu Asn Asn Gly His Arg Glu Asp Pro Ala Pro Gly Leu
 610 615 620

Leu Ser Glu Glu Leu Leu Gln Asp Glu Glu Thr Leu Leu Ser Phe Met
 625 630 635 640

Arg Asp Pro Ser Leu Arg Pro Gly Asp Pro Ala Arg Lys Ala Arg Gly
 645 650 655

Arg Thr Arg Leu Pro Ala Lys Lys Lys Pro Pro Pro Pro Pro Gln
 660 665 670

Asp Gly Pro Gly Ser Arg Thr Thr Pro Asp Lys Ala Pro Lys Lys Thr
 675 680 685

Trp Gly Gln Asp Ala Gly Ser Gly Lys Gly Gly Gln Gly Pro Pro Thr
 690 695 700

Arg Lys Pro Pro Arg Arg Thr Ser Ser His Leu Pro Ser Ser Pro Ala
 705 710 715 720

Ala Gly Asp Cys Pro Ile Leu Ala Thr Pro Glu Ser Pro Pro Pro Leu
 725 730 735

Ala Pro Glu Thr Pro Asp Glu Ala Ala Ser Val Ala Ala Asp Ser Asp
 740 745 750

Val Gln Val Pro Gly Pro Ala Ala Ser Pro Lys Pro Leu Gly Arg Leu
 755 760 765

Arg Pro Pro Arg Glu Ser Lys Val Thr Arg Arg Leu Pro Gly Ala Arg
 770 775 780

Pro Asp Ala Gly Met Gly Pro Pro Ser Ala Val Ala Glu Arg Pro Lys
785 790 795 800

Val Ser Leu His Phe Asp Thr Glu Thr Asp Gly Tyr Phe Ser Asp Gly
805 810 815

Glu Met Ser Asp Ser Asp Val Glu Ala Glu Asp Gly Gly Val Gln Arg
820 825 830

Gly Pro Arg Glu Ala Gly Ala Glu Glu Val Val Arg Met Gly Val Leu
835 840 845

Ala Ser
850

<210> 7
<211> 834
<212> PRT
<213> Homo sapiens

<400> 7

Met Glu Glu Lys Arg Arg Lys Tyr Ser Ile Ser Ser Asp Asn Ser Asp
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Thr Thr Asp Ser His Ala Thr Ser Thr Ser Ala Ser Arg Cys Ser Lys
20 25 30

Leu Pro Ser Ser Thr Lys Ser Gly Trp Pro Arg Gln Asn Glu Lys Lys
35 40 45

Pro Ser Glu Val Phe Arg Thr Asp Leu Ile Thr Ala Met Lys Ile Pro
50 55 60

Asp Ser Tyr Gln Leu Ser Pro Asp Asp Tyr Tyr Ile Leu Ala Asp Pro
65 70 75 80

Trp Arg Gln Glu Trp Glu Lys Gly Val Gln Val Pro Ala Gly Ala Glu
85 90 95

Ala Ile Pro Glu Pro Val Val Arg Ile Leu Pro Pro Leu Glu Gly Pro
100 105 110

Pro Ala Gln Ala Ser Pro Ser Ser Thr Met Leu Gly Glu Gly Ser Gln
115 120 125

Pro Asp Trp Pro Gly Gly Ser Arg Tyr Asp Leu Asp Glu Ile Asp Ala
 130 135 140

Tyr Trp Leu Glu Leu Ile Asn Ser Glu Leu Lys Glu Met Glu Arg Pro
 145 150 155 160

Glu Leu Asp Glu Leu Thr Leu Glu Arg Val Leu Glu Glu Leu Glu Thr
 165 170 175

Leu Cys His Gln Asn Met Ala Arg Ala Ile Glu Thr Gln Glu Gly Leu
 180 185 190

Gly Ile Glu Tyr Asp Glu Asp Val Val Cys Asp Val Cys Arg Ser Pro
 195 200 205

Glu Gly Glu Asp Gly Asn Glu Met Val Phe Cys Asp Lys Cys Asn Val
 210 215 220

Cys Val His Gln Ala Cys Tyr Gly Ile Leu Lys Val Pro Thr Gly Ser
 225 230 235 240

Trp Leu Cys Arg Thr Cys Ala Leu Gly Val Gln Pro Lys Cys Leu Leu
 245 250 255

Cys Pro Lys Arg Gly Gly Ala Leu Lys Pro Thr Arg Ser Gly Thr Lys
 260 265 270

Trp Val His Val Ser Cys Ala Leu Trp Ile Pro Glu Val Ser Ile Gly
 275 280 285

Cys Pro Glu Lys Met Glu Pro Ile Thr Lys Ile Ser His Ile Pro Ala
 290 295 300

Ser Arg Trp Ala Leu Ser Cys Ser Leu Cys Lys Glu Cys Thr Gly Thr
 305 310 315 320

Cys Ile Gln Cys Ser Met Pro Ser Cys Val Thr Ala Phe His Val Thr
 325 330 335

Cys Ala Phe Asp His Gly Leu Glu Met Arg Thr Ile Leu Ala Asp Asn
 340 345 350

Asp Glu Val Lys Phe Lys Ser Phe Cys Gln Glu His Ser Asp Gly Gly
 355 360 365

Pro Arg Asn Glu Pro Thr Ser Glu Pro Thr Glu Pro Ser Gln Ala Gly
 370 375 380

Glu Asp Leu Glu Lys Val Thr Leu Arg Lys Gln Arg Leu Gln Gln Leu
 385 390 395 400

Glu Glu Asp Phe Tyr Glu Leu Val Glu Pro Ala Glu Val Ala Glu Arg
 405 410 415

Leu Asp Leu Ala Glu Ala Leu Val Asp Phe Ile Tyr Gln Tyr Trp Lys
 420 425 430

Leu Lys Arg Lys Ala Asn Ala Asn Gln Pro Leu Leu Thr Pro Lys Thr
 435 440 445

Asp Glu Val Asp Asn Leu Ala Gln Gln Glu Gln Asp Val Leu Tyr Arg
 450 455 460

Arg Leu Lys Leu Phe Thr His Leu Arg Gln Asp Leu Glu Arg Val Arg
 465 470 475 480

Asn Leu Cys Tyr Met Val Thr Arg Arg Glu Arg Thr Lys His Ala Ile
 485 490 495

Cys Lys Leu Gln Glu Gln Ile Phe His Leu Gln Met Lys Leu Ile Glu
 500 505 510

Gln Asp Leu Cys Arg Glu Arg Ser Gly Arg Arg Ala Lys Gly Lys Lys
 515 520 525

Ser Asp Ser Lys Arg Lys Gly Cys Glu Gly Ser Lys Gly Ser Thr Glu
 530 535 540

Lys Lys Glu Lys Val Lys Ala Gly Pro Asp Ser Val Leu Gly Gln Leu
 545 550 555 560

Ala Gly Leu Ser Thr Ser Phe Pro Ile Asp Gly Thr Phe Phe Asn Ser
 565 570 575

Trp Leu Ala Gln Ser Val Gln Ile Thr Ala Glu Asn Met Ala Met Ser
 580 585 590

Glu Trp Pro Leu Asn Asn Gly His Arg Glu Asp Pro Ala Pro Gly Leu
 595 600 605

Leu Ser Glu Glu Leu Leu Gln Asp Glu Glu Thr Leu Leu Ser Phe Met
610 615 620

Arg Asp Pro Ser Leu Arg Pro Gly Asp Pro Ala Arg Lys Ala Arg Gly
625 630 635 640

Arg Thr Arg Leu Pro Ala Lys Lys Lys Pro Pro Pro Pro Pro Gln
645 650 655

Asp Gly Pro Gly Ser Arg Thr Thr Pro Asp Lys Ala Pro Lys Lys Thr
660 665 670

Trp Gly Gln Asp Ala Gly Ser Gly Lys Gly Gly Gln Gly Pro Pro Thr
675 680 685

Arg Lys Pro Pro Arg Arg Thr Ser Ser His Leu Pro Ser Ser Pro Ala
690 695 700

Ala Gly Asp Cys Pro Ile Leu Ala Thr Pro Glu Ser Pro Pro Pro Leu
705 710 715 720

Ala Pro Glu Thr Pro Asp Glu Ala Ala Ser Val Ala Ala Asp Ser Asp
725 730 735

Val Gln Val Pro Gly Pro Ala Ala Ser Pro Lys Pro Leu Gly Arg Leu
740 745 750

Arg Pro Pro Arg Glu Ser Lys Val Thr Arg Arg Leu Pro Gly Ala Arg
755 760 765

Pro Asp Ala Gly Met Gly Pro Pro Ser Ala Val Ala Glu Arg Pro Lys
770 775 780

Val Ser Leu His Phe Asp Thr Glu Thr Asp Gly Tyr Phe Ser Asp Gly
785 790 795 800

Glu Met Ser Asp Ser Asp Val Glu Ala Glu Asp Gly Gly Val Gln Arg
805 810 815

Gly Pro Arg Glu Ala Gly Ala Glu Glu Val Val Arg Met Gly Val Leu
820 825 830

Ala Ser

<210> 8
 <211> 329
 <212> DNA
 <213> Homo sapiens

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 cgggccgacc gtccccggcg gggggcggtg ggcctgggac gccgcgggcc cggccgcctc 180
 cctcgccgcg accccggatg gatgcgcgcc cccgcacctc ccgcgccggc cccaggagct 240
 cccggcttcg ggagcatcct tcccgcgcg gtccctgcag cggcgcgtag ccgagggcag 300
 cgcccgtcag gggggcaccg cggagcaag 329

<210> 9
 <211> 58
 <212> DNA
 <213> Homo sapiens

<400> 9
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<210> 10
 <211> 95
 <212> DNA
 <213> Homo sapiens

<400> 10
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 gctggccccg acagaacgaa aagaagccct ccgag 95

<210> 11
 <211> 158
 <212> DNA
 <213> Homo sapiens

<400> 11
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 gatgactact acatcctggc agacccatgg cgacaggaat gggagaaagg tgtgcaggtg 120
 cctgccccggg cagaggccat cccagagccc gtggtgag 158

<210> 12
 <211> 161
 <212> DNA
 <213> Homo sapiens

<400> 12
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tgagggctcc cagcctgatt ggccaggggg cagccgctat gacttggacg agattgatgc 120
ctactggctg gagctcatca actcggagct taaggagatg g 161

<210> 13
<211> 212
<212> DNA
<213> Homo sapiens

<400> 13
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aggatgttgt ctgcgacgtg tgtcgctctc ctgagggcga ggatggcaac gagatggtct 180
tctgtgacaa gtgcaacgtc tgtgtgcatc ag 212

<210> 14
<211> 168
<212> DNA
<213> Homo sapiens

<400> 14
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ggtgtccagc caaagtgcct gctctgcccc aagcgaggag gaggccttgaa gccactaga 120
agtgggacca agtgggtgca tgtcagctgt gccctatgga ttcttgag 168

<210> 15
<211> 117
<212> DNA
<213> Homo sapiens

<400> 15
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agccgctggg ctctgtcctg cagcctctgc aaggaatgca caggcacctg catccag 117

<210> 16
<211> 465
<212> DNA
<213> Homo sapiens

<400> 16
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cacagtgacg ggggcccacg taatgagccc acatctgagc ccacggaacc cagccaggct 180
ggcgaggacc tggaaaagggt gaccctgcgc aagcagcggc tgcagcagct agaggaggac 240
ttctacgagc tgggtggagcc ggctgaggtg gctgagcggc tggacctggc tgaggcactg 300

gtcgacttca tctaccagta ctggaagctg aagaggaaag ccaatgccaa ccagccgctg	360
ctgacccccca agaccgacga ggtggacaac ctggcccagc aggagcagga cgtcctctac	420
cgccgcctga agctcttcac ccattctgcg caggacctag agagg	465

<210> 17
 <211> 118
 <212> DNA
 <213> Homo sapiens

<400> 17	
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ctccaggagc agatattcca cctgcagatg aaacttattg aacaggatct gtgtcgag	118

<210> 18
 <211> 818
 <212> DNA
 <213> Homo sapiens

<400> 18	
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aggaccctgc tccagggctg ctgtcagagg aactgctgca ggacgaggag acactgctca	180
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<210> 19
 <211> 1440
 <212> DNA
 <213> Homo sapiens

<400> 19

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caacgctacc tggactcccc gccggagcca aacaactggg cgggggggtg ggggggcggc	180
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cgaaccgggc tgagccggtg cacatgacct cgcgtgggc tcacgtgcag ccggtccggt	1260
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acgcgggccc tgcacgcggg ggcagcatgc tcggctcctg gggttggagg ctctgcacaa	1380
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<210> 20
 <211> 50
 <212> DNA
 <213> Homo sapiens

<400> 20	
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<210> 21
 <211> 50

<212> DNA
 <213> Homo sapiens

 <400> 21
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 <210> 22
 <211> 50
 <212> DNA
 <213> Homo sapiens

 <400> 22
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 <210> 23
 <211> 50
 <212> DNA
 <213> Homo sapiens

 <400> 23
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